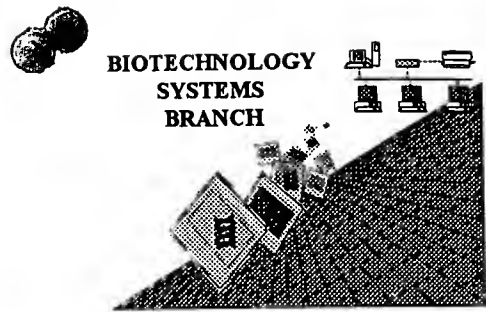


re-run *F. Hamud*

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/265,540
Art Unit / Team No. : /600
Date Processed by STIC: 3/24/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
- 7 _____ Wrong Designation
Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/265,540DATE: 03/24/1999
TIME: 16:28:51

Input Set: I265540.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Parham, Christi L.
2 Moore, Kevin W.
3 Murgolo, Nicholas J.
4 Bazan, J. Fernando
5 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
6 <130> FILE REFERENCE: DX0804
7 <140> CURRENT APPLICATION NUMBER: US/09/265,540
8 <141> CURRENT FILING DATE: 1999-03-08
9 <160> NUMBER OF SEQ ID NOS: 6
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 1381
13 <212> TYPE: DNA
14 <213> ORGANISM: primate
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (132)..(1064)
18 <400> SEQUENCE: 1
19 tgcagccacg cgtccgcgct ggcactcaga cctcagctcc aacatatgca ttctgaagaa 60
20 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaaact 120
21 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
22 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
23 1 5 10
24 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218
25 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
26 15 20 25
27 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266
28 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
29 30 35 40 45
30 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314
31 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
32 50 55 60
33 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362
34 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
35 65 70 75
36 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410
37 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
38 80 85 90
39 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458
40 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
41 95 100 105
42 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
43 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
44 110 115 120 125

Does Not Comply
Corrected Diskette Needed

see
pp 2, 3

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540

DATE: 03/24/1995
TIME: 16:28:51

Input Set: I265540.RAW

45 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
 46 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 47 130 135 140
 48 *see* ggg atg gag atc *(ncc)* aaa *(cat)* ggc ttc cac ctg gtt att gag ctg gag 602
 49 *item 10* Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
 50 145 150 155
 51 *on* gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
 52 *Ena* Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
 53 160 165 170
 54 *summary* cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
 55 *sheet* Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 56 175 180 185
 57 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
 58 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 59 190 195 200 205
 60 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
 61 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
 62 210 215 220
 63 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
 64 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
 65 225 230 235
 66 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
 67 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
 68 240 245 250
 69 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
 70 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
 71 255 260 265
 72 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
 73 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
 74 270 275 280 285
 75 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
 76 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
 77 290 295 300
 78 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
 79 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
 80 305 310
 81 ggtgaagccg agaacctggt ctgcatgaca tggaaacat gaggggacaa gttgtgtttc 1144
 82 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204
 83 *item 10* gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
 84 gwtgtgacct ctgactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
 85 *W-->* cttcaccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg 1381
 86 <210> SEQ ID NO 2
 87 <211> LENGTH: 311
 88 <212> TYPE: PRT
 89 <213> ORGANISM: primate
 90 <400> SEQUENCE: 2
 91 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
 92 1 5 10 15
 93 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
 94 20 25 30

PAGE: 3

RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540

DATE: 03/24/1991
TIME: 16:28:51

Input Set: I265540.RAW

95 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 96 35 40 45
 97 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 98 50 55 60
 99 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 100 65 70 75 80
 101 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 102 85 90 95
 103 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 104 100 105 110
 105 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 106 115 120 125
 107 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 108 130 135 140
 W--> 109 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 110 145 150 155 160
 W--> 111 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
 112 165 170 175
 113 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 114 180 185 190
 115 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 116 195 200 205
 W--> 117 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 118 210 215 220
 W--> 119 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 120 225 230 235 240
 121 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 122 245 250 255
 123 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 124 260 265 270
 125 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 126 275 280 285
 127 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 128 290 295 300
 129 Leu Leu Arg Ala Trp Ile Ser
 130 305 310
 131 <210> SEQ ID NO 3
 132 <211> LENGTH: 1244
 133 <212> TYPE: DNA
 134 <213> ORGANISM: primate
 135 <220> FEATURE:
 136 <221> NAME/KEY: CDS
 137 <222> LOCATION: (2)..(694)
 138 <400> SEQUENCE: 3
 139 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49
 140 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
 141 1 5 10 15
 142 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
 143 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 144 20 25 30

PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540

DATE: 03/24/1999
TIME: 16:28:51

Input Set: I265540.RAW

```

145      tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
146      Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
147              35              40              45
148      ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
149      Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
150              50              55              60
151      tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
152      Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
153              65              70              75              80
154      tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
155      Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
156              85              90              95
157      gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
158      Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
159              100              105              110
160      cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
161      Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
162              115              120              125
163      aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
164      Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
165              130              135              140
166      gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481
167      Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
168      145              150              155              160
169      ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529
170      Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
171              165              170              175
172      gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
173      Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
174              180              185              190
175      aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625
176      Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
177              195              200              205
178      gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
179      Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
180              210              215              220
181      caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724
182      Gln Asn Ser Gly Ala Val Cys
183      225              230
184      gaagctgctg atgtccatgt cagcaacttta tggaatccgg tctccattt tctgtcccc 784
185      aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tgggggacgac aagcttattg 844
186      atttttttct tcaaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904
187      tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgtaa 964
188      gcaaatgggc gtctggcacg cctctgacac ttttctgtca gcagccagga cagaggtcc 1024
189      cctccttgat gaagcccttc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084
190      gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144
191      aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204
192      aactttttta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244
193 <210> SEQ ID NO 4
194 <211> LENGTH: 231

```

PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540

DATE: 03/24/1999
TIME: 16:28:51

Input Set: I265540.RAW

195 <212> TYPE: PRT
196 <213> ORGANISM: primate
197 <400> SEQUENCE: 4
198 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
199 1 5 10 15
200 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
201 20 25 30
202 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
203 35 40 45
204 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
205 50 55 60
206 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
207 65 70 75 80
208 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
209 85 90 95
210 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
211 100 105 110
212 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
213 115 120 125
214 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
215 130 135 140
216 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
217 145 150 155 160
218 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
219 165 170 175
220 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
221 180 185 190
222 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
223 195 200 205
224 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
225 210 215 220
226 Gln Asn Ser Gly Ala Val Cys
227 225 230
228 <210> SEQ ID NO 5
229 <211> LENGTH: 337
230 <212> TYPE: PRT
231 <213> ORGANISM: primate
232 <400> SEQUENCE: 5
233 Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe
234 1 5 10 15
235 Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
236 20 25 30
237 Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
238 35 40 45
239 Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg
240 50 55 60
241 Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
242 65 70 75 80
243 Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
244 85 90 95

VERIFICATION SUMMARY
PATENT APPLICATION US/09/265,540DATE: 03/24/1999
TIME: 16:28:51

Input Set: I265540.RAW

Line	?	Error/Warning	Original Text
48	W	"N" or "Xaa" used: Feature required	ggg atg gag atc ncc aaa nat ggc ttc cac c
85	W	"N" or "Xaa" used: Feature required	cttcacccct tnggtccnaa gttttctcat ctgtaatg
109	W	"N" or "Xaa" used: Feature required	Ile Xaa Lys Xaa Gly Phe His Leu Val Ile G
111	W	"N" or "Xaa" used: Feature required	Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp X
117	W	"N" or "Xaa" used: Feature required	Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe S
119	W	"N" or "Xaa" used: Feature required	Xaa Val Gln Gly Glu Ala Ile Pro Leu Val L
204	W	"N" or "Xaa" used: Feature required	Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe G

Application No.: 09/2855

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

COPY FOR [] File [] Applicant